



## Exhibit C

### BLAST Analysis of SEQ ID NO:1

BLASTN 1.2.3-Paracel [2001-11-20]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: gsnMouse; humRNA

129,541 sequences; 199,339,278 total letters

Query= LEX413bestorf  
(1116 letters)

Sequences producing significant alignments:	Score (bits)	E Value
BC029118 ACCESSION:BC029118 NID:20809627 Homo sapiens Homo sa...	<u>2212</u>	0.0
AJ308569 ACCESSION:AJ308569 NID:14330408 Homo sapiens Homo sa...	<u>2204</u>	0.0
AK057808 ACCESSION:AK057808 NID:16553760 Homo sapiens Homo sa...	<u>2196</u>	0.0
AK021919 ACCESSION:AK021919 NID:10433216 Homo sapiens Homo sa...	<u>256</u>	2e-66

>BC029118 ACCESSION:BC029118 NID:20809627 Homo sapiens Homo sapiens,  
leucine-rich repeat-containing 2, clone MGC:34065  
IMAGE:5183639, mRNA, complete cds. humRNA  
Length = 1946

Score = 2212 bits (1116), Expect = 0.0  
Identities = 1116/1116 (100%)  
Strand = Plus / Plus

Query: 1	atgggacataaaagtgggtgtcttcgacatttctgtcatcagagccttggtgggaaactcgt	60
Sbjct: 166	atgggacataaaagtgggtgtcttcgacatttctgtcatcagagccttggtgggaaactcgt	225
Query: 61	gtcaagaagcacaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg	120
Sbjct: 226	gtcaagaagcacaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg	285
Query: 121	gagaagataaaggaggaggtggaactttgtggccgaatgcaggaggaagggcatccccag	180
Sbjct: 286	gagaagataaaggaggaggtggaactttgtggccgaatgcaggaggaagggcatccccag	345
Query: 181	gctgtatactgcaagaatggcttcatagacaccagcgtgcggttcttgacaagattgaa	240
Sbjct: 346	gctgtatactgcaagaatggcttcatagacaccagcgtgcggttcttgacaagattgaa	405
Query: 241	aggaacactctcacaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcg	300

Sbjct: 406 |||||  
 aggaacactctcacaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcg 465

Query: 301 tttgtggttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 360  
 Sbjct: 466 tttgtggttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 525

Query: 361 acacacctgagagaatggtacataagcaataccttgattcaaatacttctacatatatt 420  
 Sbjct: 526 acacacctgagagaatggtacataagcaataccttgattcaaatacttctacatatatt 585

Query: 421 cagttatttcaagcgatgagaattctggatctgcaaaaaaccaaatactcacatcttcca 480  
 Sbjct: 586 cagttatttcaagcgatgagaattctggatctgcaaaaaaccaaatactcacatcttcca 645

Query: 481 gcagaaatcgggtgttgaagaacctgaaagaactcaatgtgggttcaactatctgaag 540  
 Sbjct: 646 gcagaaatcgggtgttgaagaacctgaaagaactcaatgtgggttcaactatctgaag 705

Query: 541 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 600  
 Sbjct: 706 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 765

Query: 601 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 660  
 Sbjct: 766 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 825

Query: 661 atctcagcaacaagttttccagtgtcccaatctgtgtcctgcggatgtcgaatttgcag 720  
 Sbjct: 826 atctcagcaacaagttttccagtgtcccaatctgtgtcctgcggatgtcgaatttgcag 885

Query: 721 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 780  
 Sbjct: 886 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 945

Query: 781 gagctgcagagctttctcttgataaaaaacaagttgacctaccttccctattccatgctg 840  
 Sbjct: 946 gagctgcagagctttctcttgataaaaaacaagttgacctaccttccctattccatgctg 1005

Query: 841 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggaggagctcccaact 900  
 Sbjct: 1006 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggaggagctcccaact 1065

Query: 901 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 960  
 Sbjct: 1066 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 1125

Query: 961 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1020  
|||||  
Sbjct: 1126 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1185

Query: 1021 gataaagaagttatgaaagcctatatattgaagaccttaaagaaagagaatctgttcccagc 1080  
|||||  
Sbjct: 1186 gataaagaagttatgaaagcctatatattgaagaccttaaagaaagagaatctgttcccagc 1245

Query: 1081 tataaccaccaaagtgtcttttagccttcaactttga 1116  
|||||  
Sbjct: 1246 tataaccaccaaagtgtcttttagccttcaactttga 1281

>AJ308569 ACCESSION:AJ308569 NID:14330408 Homo sapiens Homo sapiens  
mRNA for leucine-rich repeat-containing 2 protein (LRRC2  
gene). humRNA  
Length = 4860

Score = 2204 bits (1112), Expect = 0.0  
Identities = 1115/1116 (99%)  
Strand = Plus / Plus

Query: 1 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 60  
|||||  
Sbjct: 168 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 227

Query: 61 gtcaagaagcacaaagccttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 120  
|||||  
Sbjct: 228 gtcaagaagcacaaagccttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 287

Query: 121 gagaagataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccag 180  
|||||  
Sbjct: 288 gagaagataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccag 347

Query: 181 gctgtatactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaa 240  
|||||  
Sbjct: 348 gctgtatactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaa 407

Query: 241 aggaacactctcacaaggcagagttcacttccaaggacagaggcaaacgggagcagtgcg 300  
|||||  
Sbjct: 408 aggaacactctcacaaggcagagttcacttccaaggacagaggcaaacgggagcagtgcg 467

Query: 301 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 360  
|||||  
Sbjct: 468 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 527

Query: 361 acacacctgagagaatggtacataagcaataccttgattcaaatcattcctacatatatt 420  
 |||  
 Sbjct: 528 acacacctgagagaatggtacataagcaataccttgattcaaatcattcctacatatatt 587

Query: 421 cagttatttcaagcgatgagaattctggatctgccaaaaaaccaatctcacatcttcca 480  
 |||  
 Sbjct: 588 cagttatttcaagagatgagaattctggatctgccaaaaaaccaatctcacatcttcca 647

Query: 481 gcagaaatcggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 540  
 |||  
 Sbjct: 648 gcagaaatcggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 707

Query: 541 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 600  
 |||  
 Sbjct: 708 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 767

Query: 601 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 660  
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 Sbjct: 768 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 827

Query: 661 atctcagcaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 720  
 |||  
 Sbjct: 828 atctcagcaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 887

Query: 721 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 780  
 |||  
 Sbjct: 888 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 947

Query: 781 gagctgcagagctttctcttgataaaaaacaagttgacctaccttcctattccatgctg 840  
 |||  
 Sbjct: 948 gagctgcagagctttctcttgataaaaaacaagttgacctaccttcctattccatgctg 1007

Query: 841 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggtggagctcccaact 900  
 |||  
 Sbjct: 1008 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggtggagctcccaact 1067

Query: 901 gccctttgtgactcatccacacctttaaatttgtaagccttatggacaatcctattgat 960  
 |||  
 Sbjct: 1068 gccctttgtgactcatccacacctttaaatttgtaagccttatggacaatcctattgat 1127

Query: 961 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1020  
 |||  
 Sbjct: 1128 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1187

Query: 1021 gataaagaagttatgaaagcctatattgaagaccttaagaaagagaatctgttcccagc 1080

Sbjct: 1188 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
gataaagaagttatgaaagcctatattgaagaccttaaagaaagagaatctgttcccagc 1247

Query: 1081 tataaccaccaaagtgtcttttagccttcaactttga 1116

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Sbjct: 1248 tataaccaccaaagtgtcttttagccttcaactttga 1283